Untitled
Title: US-10-615-383A-7_COPY_252_1895
Perfect score: 1644
Sequence: 1 gagaatacagtacaagacgt.....acttgcctcctgaaaaaact 1644

RESULT 3
ABN93014
ID ABN93014 standard; DNA; 2793 BP.
XX
AC ABN93014;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2477.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy; gene; ds.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-0055779P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2002-381255/41.
DR P-PSDB; ABP40469.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 2477; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site
XX
SQ Sequence 2793 BP; 1149 A; 423 C; 497 G; 724 T; 0 U; 0 Other;

Query Match 100.0%; Score 1644; DB 1; Length 2793;
Best Local Similarity 100.0%;
Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAATACAGTACAAGACGTTAAAGATTCGAATATGGATGATGAATTATCAGATAGCAAT 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 151 GAGAATACAGTACAAGACGTTAAAGATTCGAATATGGATGATGAATTATCAGATAGCAAT 210

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Qy        61 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 120
Db       211 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 270

Qy       121 GATGATGATAACCAAATAAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 180
Db       271 GATGATGATAACCAAATAAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 330

Qy       181 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAACGAAGCAACATTTTTACAA 240
Db       331 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAACGAAGCAACATTTTTACAA 390

Qy       241 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCTCATCAGTC 300
Db       391 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCTCATCAGTC 450

Qy       301 GAATCCTCAAATTCATCAATGGATACTGCCCAACAACCATCTCATACAACAATAAATAGT 360
Db       451 GAATCCTCAAATTCATCAATGGATACTGCCCAACAACCATCTCATACAACAATAAATAGT 510

Qy       361 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 420
Db       511 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 570

Qy       421 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 480
Db       571 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 630

Qy       481 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 540
Db       631 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 690

Qy       541 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 600
Db       691 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 750

Qy       601 AGACCGTTATCTACAACATCTGCCCAACCATCGAGTAAGCGTGTAACCGTAAATCAATTA 660
Db       751 AGACCGTTATCTACAACATCTGCCCAACCATCGAGTAAGCGTGTAACCGTAAATCAATTA 810

Qy       661 GCGGCAGAACAAGGTTCGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 720
Db       811 GCGGCAGAACAAGGTTCGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 870

Qy       721 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACTTAATCTAT 780
Db       871 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACTTAATCTAT 930

Qy       781 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 840
Db       931 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 990

Qy       841 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAATAAAAGAT 900
Db       991 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAATAAAAGAT 1050

Qy       901 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 960
Db      1051 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 1110

Qy       961 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1020
Db      1111 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1170
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Qy       1021 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1230

Qy       1081 GCCCTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 GCCCTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1290

Qy       1141 ACTGCTAACCTTCAAAGTATGTTCACAAACATAGATACGAAAAACCATACAGTTGAGCAA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 ACTGCTAACCTTCAAAGTATGTTCACAAACATAGATACGAAAAACCATACAGTTGAGCAA 1350

Qy       1201 ACGATTTATATTAACCCTCTTCGTTATTCAGCCAAAGAAACAAATGTAAATATTTCAGGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 ACGATTTATATTAACCCTCTTCGTTATTCAGCCAAAGAAACAAATGTAAATATTTCAGGG 1410

Qy       1261 AATGGCGATGAAGGTTCAACAATTATCGACGATAGTACAATCATTAAAGTTTATAAGGTT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AATGGCGATGAAGGTTCAACAATTATCGACGATAGTACAATCATTAAAGTTTATAAGGTT 1470

Qy       1321 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1530

Qy       1381 GTCACAAATGATGATTATGCCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 GTCACAAATGATGATTATGCCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1590

Qy       1441 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGACCCTAATAAGGACGAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGACCCTAATAAGGACGAT 1650

Qy       1501 TACACGACGATACAGCAAACTGTGACAATGCAAACGACTATAAATGAGTATACTGGTGAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 TACACGACGATACAGCAAACTGTGACAATGCAAACGACTATAAATGAGTATACTGGTGAG 1710

Qy       1561 TTTAGAACAGCATCCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1620
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Db       1711 TTTAGAACAGCATCCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1770

Qy       1621 GGTGACTTGCCTCCTGAAAAAACT 1644
             ||||||||||||||||||||||||
Db       1771 GGTGACTTGCCTCCTGAAAAAACT 1794
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Title:            US-10-615-383A-7
Perfect score:    2976
Sequence:         1 atattgcaaaaaagacttat.....ccaacaaatataaggtgttg 2976
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RESULT 4
US-09-134-001C-2477
;  Sequence 2477, Application US/09134001C
;  Patent No. 6380370
;  GENERAL INFORMATION:
;    APPLICANT: Lynn Doucette-Stamm et al
;    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLCCCCCUS
;    TITLE OF INVENTION:   EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;    FILE REFERENCE: GTC-007
;    CURRENT APPLICATION NUMBER: US/09/134,001C
;    CURRENT FILING DATE:   1998-08-13
;    PRIOR APPLICATION NUMBER: US 60/064,964
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; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2477
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2477

Query Match 93.8%; Score 2791.4; DB 3; Length 2793;
Best Local Similarity 99.9%;
Matches 2792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        102 TTAAAAAAAAAATAATTTACTAACTAAAAAGAAACCTATAGCAAATAAATCCAATAAATAT 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAAAAAAAAAATAATTTACTAACTAAAAAGAAACCTATAGCAAATAAATCCAATAAATAT 60

Qy        162 GCAATTAGAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAGCATTATTGTTT 221
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 GCAATTAGAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAACATTATTGTTT 120

Qy        222 GGTTTAGGTCATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTCG 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTTTAGGTCATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTCG 180

Qy        282 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT 240

Qy        342 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAAGAAGAA 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAAGAAGAA 300

Qy        402 ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT 360

Qy        462 GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA 420

Qy        522 GAAGAAGTGGTAAAAGAACCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAAGAAGTGGTAAAAGAACCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC 480

Qy        582 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 540

Qy        642 GAAAATTCCCGCGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAATTCCCGCGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC 600

Qy        702 AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT 761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT 660

Qy        762 CAACCGTCTAGCTATAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT 821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACCGTCTAGCTATAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT 720

Qy        822 TTACCAATAAATGAATATGAAAATAAGGTTAGACCGTTATCTACAACATCTGCCCAACCA 881
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Db 721 TTACCAATAAATGAATATGAAAATAAGGTTAGACCGTTATCTACAACATCTGCCCAACCA 780

Qy 882 TCGAGTAAGCGTGTAACCGTAAATCAATTAGCGGCAGAACAAGGTTCGAATGTTAATCAT 941

Db 781 TCGAGTAAGCGTGTAACCGTAAATCAATTAGCGGCAGAACAAGGTTCGAATGTTAATCAT 840

Qy 942 TTAATTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 1001

Db 841 TTAATTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 900

Qy 1002 AAAGCACATGATGCTGAAAACTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 1061

Db 901 AAAGCACATGATGCTGAAAACTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 960

Qy 1062 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCCATCAGATTTAACC 1121

Db 961 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCCATCAGATTTAACC 1020

Qy 1122 GATAGTTTTGCAATACCAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTACT 1181

Db 1021 GATAGTTTTGCAATACCAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTACT 1080

Qy 1182 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1241

Db 1081 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1140

Qy 1242 AATATTAAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1301

Db 1141 AATATTAAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1200

Qy 1302 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTCATCAGTAAATAAAACAATTACG 1361

Db 1201 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTCATCAGTAAATAAAACAATTACG 1260

Qy 1362 GTTGAATATCAAAAACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTCACAAAC 1421

Db 1261 GTTGAATATCAAAAACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTCACAAAC 1320

Qy 1422 ATAGATACGAAAAACCATACAGTTGAGCAAACGATTTATATTAACCCTCTTCGTTATTCA 1481

Db 1321 ATAGATACGAAAAACCATACAGTTGAGCAAACGATTTATATTAACCCTCTTCGTTATTCA 1380

Qy 1482 GCCAAAGAAACAAATGTAAATATTTCAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1541

Db 1381 GCCAAAGAAACAAATGTAAATATTTCAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1440

Qy 1542 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1601

Db 1441 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1500

Qy 1602 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTAGGA 1661

Db 1501 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTAGGA 1560

Qy 1662 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCACCATATATTATTAAAGTT 1721

Db 1561 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCACCATATATTATTAAAGTT 1620

Qy 1722 ATTAGTAAATATGACCCTAATAAGGACGATTACACGACGATACAGCAAACTGTGACAATG 1781

Db 1621 ATTAGTAAATATGACCCTAATAAGGACGATTACACGACGATACAGCAAACTGTGACAATG 1680

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Qy       1782 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATCCTATGATAATACAATT 1841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATCCTATGATAATACAATT 1740

Qy       1842 GCTTTCTCTACAAGTTCAGGTCAAGGACAAGGTGACTTGCCTCCTGAAAAAACTTATAAA 1901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GCTTTCTCTACAAGTTCAGGTCAAGGACAAGGTGACTTGCCTCCTGAAAAAACTTATAAA 1800

Qy       1902 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1860

Qy       1962 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAATCA 2021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAATCA 1920

Qy       2022 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAAACGGATTGACTTAT 2081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAAACGGATTGACTTAT 1980

Qy       2082 AAAATTACATTCGAAACACCGGAAGGATATACGCCGACGCTTAAACATTCAGGAACAAAT 2141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AAAATTACATTCGAAACACCGGAAGGATATACGCCGACGCTTAAACATTCAGGAACAAAT 2040

Qy       2142 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAACGGACAAGACGATATG 2201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAACGGACAAGACGATATG 2100

Qy       2202 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAACTATGTATGGTAT 2261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAACTATGTATGGTAT 2160

Qy       2262 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2220

Qy       2322 ACGTTAAAAAGATGAAAACGGAAATATCATTAGTACAACAACAACTGATGAAAATGGAAAG 2381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 ACGTTAAAAAGATGAAAACGGAAATATCATTAGTACAACAACAACTGATGAAAATGGAAAG 2280

Qy       2382 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2340

Qy       2442 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGGAAGAA 2501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGGAAGAA 2400

Qy       2502 GTCCATGTAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GTCCATGTAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2460

Qy       2562 GACTCAGATTCAGATAGTGATTCAGACTCAGATAGCGACGACTCAGACTCCGATAGCGAT 2621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GACTCAGATTCAGATAGTGATTCAGACTCAGATAGCGACGACTCAGACTCCGATAGCGAT 2520

Qy       2622 TCCGACTCAGACAGCGACTCAGATTCCGATAGTGATTCAGATTCAGACAGTGACTCAGAC 2681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TCCGACTCAGACAGCGACTCAGATTCCGATAGTGATTCAGATTCAGACAGTGACTCAGAC 2580

Qy       2682 TCAGATAGTGATTCAGATTCAGACAGCGATTCCGACTCAGACAGTGACTCAGGATTAGAC 2741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TCAGATAGTGATTCAGATTCAGACAGCGATTCCGACTCAGACAGTGACTCAGGATTAGAC 2640
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Qy        2742 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2700

Qy        2802 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2760

Qy        2862 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2894
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Db        2761 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2793
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Title: US-10-615-383A-10
Perfect score: 4824
Sequence: 1 LKKNNLLTKKKPIANKSNKY.....FAGLGALLLGKRRKNRKNKN 930

RESULT 3
ABP40469
ID ABP40469 standard; protein; 930 AA.
XX
AC ABP40469;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-0055779P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2002-381255/41.
DR N-PSDB; ABN93014.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 5314; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 99.9%; Score 4820; DB 1; Length 930;
Best Local Similarity 99.9%;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGAALLFGLGHNEAKAEENTVQDVKDS 60
Db    1 LKKNNLLTKKKPIANKSNKYAIRKFTVGTASIVIGATLLFGLGHNEAKAEENTVQDVKDS 60

Qy   61 NMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN 120
Db   61 NMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENRSKDITQSTTN 120

Qy  121 VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE 180
Db  121 VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINSEASIQTSDNE 180

Qy  181 ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN 240
Db  181 ENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDEKISNQDELLN 240

Qy  241 LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII 300
Db  241 LPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSDGII 300

Qy  301 KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT 360
Db  301 KAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNSGEIIATGT 360

Qy  361 YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT 420
Db  361 YDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTIT 420

Qy  421 VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID 480
Db  421 VEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNGDEGSTIID 480

Qy  481 DSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV 540
Db  481 DSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFGNIDSPYIIKV 540

Qy  541 ISKYDPNKDDYTTIQQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGDLPPEKTYK 600
Db  541 ISKYDPNKDDYTTIQQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQGQGDLPPEKTYK 600

Qy  601 IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLTY 660
Db  601 IGDYVWEDVDKDGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLTY 660

Qy  661 KITFETPEGYTPTLKHSGTNPALDSEGNSVWWTINGQDDMTIDSGFYQTPKYSLGNYVWY 720
Db  661 KITFETPEGYTPTLKHSGTNPALDSEGNSVWWTINGQDDMTIDSGFYQTPKYSLGNYVWY 720

Qy  721 DTNKDGIQGDDEKGISGVKVTLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG 780
Db  721 DTNKDGIQGDDEKGISGVKVTLKDENGNIISTTTTDENGKYQFDNLNSGNYIVHFDKPSG 780

Qy  781 MTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYYDDDSDSDSDSDSDSDDSDSDSD 840
Db  781 MTQTTTDSGDDDEQDADGEEVHVTITDHDDFSIDNGYYDDDSDSDSDSDSDSDDSDSDSD 840
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Qy          841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 900

Qy          901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930
                |||||||||||||||||||||||||||||
Db          901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930


Title:          US-10-615-383A-10_COPY_51_598
Perfect score:  2808
Sequence:       1 ENTVQDVKDSNMDDELSDSN.........TIAFSTSSGQGQGDLPPEKT 548


RESULT 4
ABP40469
ID   ABP40469 standard; protein; 930 AA.
XX
AC   ABP40469;
XX
DT   24-JUL-2002  (first entry)
XX
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW   antibacterial; gene therapy.
XX
OS   Staphylococcus epidermidis.
XX
PN   US6380370-B1.
XX
PD   30-APR-2002.
XX
PF   13-AUG-1998;    98US-00134001.
XX
PR   14-AUG-1997;    97US-0055779P.
PR   08-NOV-1997;    97US-0064964P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2002-381255/41.
DR   N-PSDB; ABN93014.
XX
PT   Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT   polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS   Disclosure; SEQ ID NO 5314; 267pp; English.
XX
CC   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC   frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC   given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC   antibacterial activity and can be used in gene therapy. The sequences can
CC   also be used in the diagnosis and treatment of bacterial infections,
CC   particularly S. epidermidis infections. The sequences can be used to
CC   screen for compounds able to interfere with the S. epidermidis life cycle
CC   or inhibit S. epidermidis infection. N.B. The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from the USPTO web site
XX
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SQ Sequence 930 AA;

Query Match 100.0%; Score 2808; DB 1; Length 930;
Best Local Similarity 100.0%;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ENTVQDVKDSNMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ENTVQDVKDSNMDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENR 110

Qy         61 SKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINS 120
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 SKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTINS 170

Qy        121 EASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDE 180
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 EASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDE 230

Qy        181 KISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSIT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 KISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSIT 290

Qy        241 EGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKD 300
              |||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        291 EGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKD 350

Qy        301 NSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 NSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKT 410

Qy        361 ALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISG 420
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 ALSSVNKTITVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISG 470

Qy        421 NGDEGSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFG 480
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 NGDEGSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEDVTNDDYAQLGNNNDVNINFG 530

Qy        481 NIDSPYIIKVISKYDPNKDDYTTIQQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQGQ 540
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 NIDSPYIIKVISKYDPNKDDYTTIQQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQGQ 590

Qy        541 GDLPPEKT 548
              ||||||||
Db        591 GDLPPEKT 598
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